

- (ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or
 - (iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii).
7. The polynucleotide according to claim 6, further comprising
- (i) functionally neutral sense mutations in (i).
8. The polynucleotide according to claim 6, wherein hybridization is carried out with a stringency corresponding to at most 2x SSC.
9. The polynucleotide sequence according to claim 1, which codes for a polypeptide containing the amino acid sequence shown in SEQ ID no. 2.
10. A Coryneform bacteria in which the *ilvE* gene is enhanced.
11. The Coryneform bacteria according to claim 10, wherein the *ilvE* gene is over-expressed.
12. A method for the fermentative preparation of L-amino acids in coryneform bacteria, comprising:
- a) fermenting, in a medium, the coryneform bacteria which produce the desired L-amino acid and in which at least the endogenous *ilvE* gene or nucleotide sequences which code for it are enhanced.
13. The method according to claim 12, further comprising:
- b) concentrating the L-amino acid in the medium or in the cells of the bacteria.
14. The method according to claim 13, further comprising:

123	456	789	1011	1213	1415	1617	1819	2021	2223	2425	2627	2829	3031	3233	3435	3637	3839	4041	4243	4445	4647	4849	5051	5253	5455	5657	5859	6061	6263	6465	6667	6869	7071	7273	7475	7677	7879	8081	8283	8485	8687	8889	9091	9293	9495	9697	9899	100101	102103	104105	106107	108109	110111	112113	114115	116117	118119	120121	122123	124125	126127	128129	130131	132133	134135	136137	138139	140141	142143	144145	146147	148149	150151	152153	154155	156157	158159	160161	162163	164165	166167	168169	170171	172173	174175	176177	178179	180181	182183	184185	186187	188189	190191	192193	194195	196197	198199	200201	202203	204205	206207	208209	210211	212213	214215	216217	218219	220221	222223	224225	226227	228229	230231	232233	234235	236237	238239	240241	242243	244245	246247	248249	250251	252253	254255	256257	258259	260261	262263	264265	266267	268269	270271	272273	274275	276277	278279	280281	282283	284285	286287	288289	290291	292293	294295	296297	298299	300301	302303	304305	306307	308309	310311	312313	314315	316317	318319	320321	322323	324325	326327	328329	330331	332333	334335	336337	338339	340341	342343	344345	346347	348349	350351	352353	354355	356357	358359	360361	362363	364365	366367	368369	370371	372373	374375	376377	378379	380381	382383	384385	386387	388389	390391	392393	394395	396397	398399	400401	402403	404405	406407	408409	410411	412413	414415	416417	418419	420421	422423	424425	426427	428429	430431	432433	434435	436437	438439	440441	442443	444445	446447	448449	450451	452453	454455	456457	458459	460461	462463	464465	466467	468469	470471	472473	474475	476477	478479	480481	482483	484485	486487	488489	490491	492493	494495	496497	498499	500501	502503	504505	506507	508509	510511	512513	514515	516517	518519	520521	522523	524525	526527	528529	530531	532533	534535	536537	538539	540541	542543	544545	546547	548549	550551	552553	554555	556557	558559	560561	562563	564565	566567	568569	570571	572573	574575	576577	578579	580581	582583	584585	586587	588589	590591	592593	594595	596597	598599	600601	602603	604605	606607	608609	610611	612613	614615	616617	618619	620621	622623	624625	626627	628629	630631	632633	634635	636637	638639	640641	642643	644645	646647	648649	650651	652653	654655	656657	658659	660661	662663	664665	666667	668669	670671	672673	674675	676677	678679	680681	682683	684685	686687	688689	690691	692693	694695	696697	698699	700701	702703	704705	706707	708709	710711	712713	714715	716717	718719	720721	722723	724725	726727	728729	730731	732733	734735	736737	738739	740741	742743	744745	746747	748749	750751	752753	754755	756757	758759	760761	762763	7647
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15. The method according to claim 12, wherein the L amino acids are L-lysine, L-valine. L-isoleucine and/or L-phenylalanine.
16. The method according to claim 12, wherein ilvE gene or nucleotide sequences coding for this gene are overexpressed.
17. The method according to claim 12, wherein additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced in the bacteria.
18. The method according to claim 12, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
19. The method according to claim 12, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the ilvE gene.
20. The method according to claim 12, wherein the expression of the polynucleotide(s) which code(s) for the ilvE gene is enhanced.
21. The method according to claim 20, wherein the expression of the polynucleotide(s) which code(s) for the ilvE gene is over-expressed.
22. The method according to claim 12, wherein the regulatory or catalytic properties of the polypeptide for which the polynucleotide ilvE codes are increased.
23. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced or overexpressed; wherein the

[illegible]

the dapA gene which codes for dihydrodipicolinate synthase,

the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

the tpi gene which codes for triose phosphate isomerase,

the pgk gene which codes for 3-phosphoglycerate kinase,

the zwf gene which codes for glucose 6-phosphate dehydrogenase,

the *pyc* gene which codes for pyruvate carboxylase,

the mgo gene which codes for malate-quinone oxidoreductase,

the lysC gene which codes for a feed-back resistant aspartate kinase,

the *lysE* gene which codes for lysine export,

the hom gene which codes for homoserine dehydrogenase

the *ilvA* gene which codes for threonine dehydratase or the *ilvA*(Fbr) allele which codes for a feed back resistant threonine dehydratase,

the *ilvBN* gene which codes for acetohydroxy-acid synthase,

the *ilvD* gene which codes for dihydroxy-acid dehydratase, and

the *zw1* gene which codes for the Zw1 protein.

24. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the genes are selected from the group consisting of:
- the pck gene which codes for phosphoenol pyruvate carboxykinase,
- the pgi gene which codes for glucose 6-phosphate isomerase,
- the poxB gene which codes for pyruvate oxidase, and
- the zwa2 gene which codes for the Zwa2 protein.
25. The method according to claim 12, wherein microorganisms of the species *Corynebacterium glutamicum* are employed.
26. A Coryneform bacteria, comprising a vector which carries a polynucleotide according to claim 1.
27. A method for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes which code for transaminase E or have a high similarity with the sequence of the *ilvE* gene, comprising contacting the RNA, cDNA, or DNA with hybridization probes comprising polynucleotide sequences according to claim 1.
28. The method according to claim 27, wherein arrays, micro arrays or DNA chips are employed.